

SEQUENCE LISTING

<110> CHIEN, David Y.
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<120> HCV ANTIGEN/ANTIBODY COMBINATION ASSAY

<130> 2302-16073 / PP16073.003

<140> 09/881,239

<141> 2001-06-14

<160> 8

<170> PatentIn Ver. 2.0

<210> 1

<211> 728

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:
 representative NS3/4a conformational antigen

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			20					25					30	Pro
Gly	Leu	Asp	Gly	Ile	Cys	Ser	Ile	Glu	Glu	Phe	Ala	Pro	Ile	Thr
		35					40					45		Ala
Tyr	Ala	Gln	Gln	Thr	Arg	Gly	Leu	Leu	Gly	Cys	Ile	Ile	Thr	Ser
	50					55					60			Leu
Thr	Gly	Arg	Asp	Lys	Asn	Gln	Val	Glu	Gly	Glu	Val	Gln	Ile	Val
65					70					75				80
Thr	Ala	Ala	Gln	Thr	Phe	Leu	Ala	Thr	Cys	Ile	Asn	Gly	Val	Cys
			85						90					95
Thr	Val	Tyr	His	Gly	Ala	Gly	Thr	Arg	Thr	Ile	Ala	Ser	Pro	Lys
			100					105					110	Gly
Pro	Val	Ile	Gln	Met	Tyr	Thr	Asn	Val	Asp	Gln	Asp	Leu	Val	Gly
			115				120						125	Trp

Pro Ala Ser Gln Gly Thr Arg Ser Leu Thr Pro Cys Thr Cys Gly Ser
 130 135 140

Ser Asp Leu Tyr Leu Val Thr Arg His Ala Asp Val Ile Pro Val Arg
 145 150 155 160

Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu Ser Pro Arg Pro Ile Ser
 165 170 175

Tyr Leu Lys Gly Ser Ala Gly Gly Pro Leu Leu Cys Pro Ala Gly His
 180 185 190

Ala Val Gly Ile Phe Arg Ala Ala Val Cys Thr Arg Gly Val Ala Lys
 195 200 205

Ala Val Asp Phe Ile Pro Val Glu Asn Leu Glu Thr Thr Met Arg Ser
 210 215 220

Pro Val Phe Thr Asp Asn Ser Ser Pro Pro Val Val Pro Gln Ser Phe
 225 230 235 240

Gln Val Ala His Leu His Ala Pro Thr Gly Ser Gly Lys Ser Thr Lys
 245 250 255

Val Pro Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val Leu Val Leu Asn
 260 265 270

Pro Ser Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr Met Ser Lys Ala
 275 280 285

His Gly Ile Asp Pro Asn Ile Arg Thr Gly Val Arg Thr Ile Thr Thr
 290 295 300

Gly Ser Pro Ile Thr Tyr Ser Thr Tyr Gly Lys Phe Leu Ala Asp Gly
 305 310 315 320

Gly Cys Ser Gly Gly Ala Tyr Asp Ile Ile Ile Cys Asp Glu Cys His
 325 330 335

Ser Thr Asp Ala Thr Ser Ile Leu Gly Ile Gly Thr Val Leu Asp Gln
 340 345 350

Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu Ala Thr Ala Thr Pro
 355 360 365

Pro Gly Ser Val Thr Val Pro His Pro Asn Ile Glu Glu Val Ala Leu
 370 375 380

Ser Thr Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala Ile Pro Leu Glu
 385 390 395 400

Val Ile Lys Gly Gly Arg His Leu Ile Phe Cys His Ser Lys Lys Lys
 405 410 415

Cys Asp Glu Leu Ala Ala Lys Leu Val Ala Leu Gly Ile Asn Ala Val
 420 425 430
 Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val Ile Pro Pro Ile Gly Asp
 435 440 445
 Val Val Val Val Ala Thr Asp Ala Leu Met Thr Gly Tyr Thr Gly Asp
 450 455 460
 Phe Asp Ser Val Ile Asp Cys Asn Thr Cys Val Thr Gln Thr Val Asp
 465 470 475 480
 Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu Thr Ile Thr Leu Pro Gln
 485 490 495
 Asp Ala Val Ser Arg Thr Gln Arg Arg Gly Arg Thr Gly Arg Gly Lys
 500 505 510
 Pro Gly Ile Tyr Arg Phe Val Ala Pro Gly Glu Arg Pro Ser Gly Met
 515 520 525
 Phe Asp Ser Ser Val Leu Cys Glu Cys Tyr Asp Ala Gly Cys Ala Trp
 530 535 540
 Tyr Glu Leu Thr Pro Ala Glu Thr Thr Val Arg Leu Arg Ala Tyr Met
 545 550 555 560
 Asn Thr Pro Gly Leu Pro Val Cys Gln Asp His Leu Glu Phe Trp Glu
 565 570 575
 Gly Val Phe Thr Gly Leu Thr His Ile Asp Ala His Phe Leu Ser Gln
 580 585 590
 Thr Lys Gln Ser Gly Glu Asn Leu Pro Tyr Leu Val Ala Tyr Gln Ala
 595 600 605
 Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser Trp Asp Gln Met
 610 615 620
 Trp Lys Cys Leu Ile Arg Leu Lys Pro Thr Leu His Gly Pro Thr Pro
 625 630 635 640
 Leu Leu Tyr Arg Leu Gly Ala Val Gln Asn Glu Ile Thr Leu Thr His
 645 650 655
 Pro Val Thr Lys Tyr Ile Met Thr Cys Met Ser Ala Asp Leu Glu Val
 660 665 670
 Val Thr Ser Thr Trp Val Leu Val Gly Gly Val Leu Ala Ala Leu Ala
 675 680 685
 Ala Tyr Cys Leu Ser Thr Gly Cys Val Val Ile Val Gly Arg Val Val
 690 695 700

Leu Ser Gly Lys Pro Ala Ile Ile Pro Asp Arg Glu Val Leu Tyr Arg
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Glu Phe Asp Glu Met Glu Glu Cys
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<210> 2
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 representative NS3/4a conformational antigen

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 <222> (1)..(2058)

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 tgc ata atc acc agc cta act ggc cgg gac aaa aac caa gtg gag ggt 96
 Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu Gly
 20 25 30
 gag gtc cag att gtg tca act gct gcc caa acc ttc ctg gca acg tgc 144
 Glu Val Gln Ile Val Ser Thr Ala Ala Gln Thr Phe Leu Ala Thr Cys
 35 40 45
 atc aat ggg gtg tgc tgg act gtc tac cac ggg gcc gga acg agg acc 192
 Ile Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Thr Arg Thr
 50 55 60
 atc gcg tca ccc aag ggt cct gtc atc cag atg tat acc aat gta gac 240
 Ile Ala Ser Pro Lys Gly Pro Val Ile Gln Met Tyr Thr Asn Val Asp
 65 70 75 80
 caa gac ctt gtg ggc tgg ccc gct ccg caa ggt agc cga tca ttg aca 288
 Gln Asp Leu Val Gly Trp Pro Ala Pro Gln Gly Ser Arg Ser Leu Thr
 85 90 95
 ccc tgc act tgc ggc tcc tcg gac ctt tac ctg gtc acg agg cac gcc 336
 Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala
 100 105 110
 gat gtc att ccc gtg cgc cgg cgg ggt gat agc agg ggc agc ctg ctg 384
 Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu
 115 120 125
 tcg ccc cgg ccc att tcc tac ttg aaa ggc tcc tcg ggg ggt ccg ctg 432

Ser	Pro	Arg	Pro	Ile	Ser	Tyr	Leu	Lys	Gly	Ser	Ser	Gly	Gly	Pro	Leu		
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Leu	Cys	Pro	Ala	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala	Val	Cys		
145					150					155					160		
acc	cgt	gga	gtg	gct	aag	gcg	gtg	gac	ttt	atc	cct	gtg	gag	aac	cta	528	
Thr	Arg	Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Ile	Pro	Val	Glu	Asn	Leu		
				165					170					175			
gag	aca	acc	atg	agg	tcc	ccg	gtg	ttc	acg	gat	aac	tcc	tct	cca	cca	576	
Glu	Thr	Thr	Met	Arg	Ser	Pro	Val	Phe	Thr	Asp	Asn	Ser	Ser	Pro	Pro		
			180					185					190				
gta	gtg	ccc	cag	agc	ttc	cag	gtg	gct	cac	ctc	cat	gct	ccc	aca	ggc	624	
Val	Val	Pro	Gln	Ser	Phe	Gln	Val	Ala	His	Leu	His	Ala	Pro	Thr	Gly		
		195					200					205					
agc	ggc	aaa	agc	acc	aag	gtc	ccg	gct	gca	tat	gca	gct	cag	ggc	tat	672	
Ser	Gly	Lys	Ser	Thr	Lys	Val	Pro	Ala	Ala	Tyr	Ala	Ala	Gln	Gly	Tyr		
	210					215					220						
aag	gtg	cta	gta	ctc	aac	ccc	tct	gtt	gct	gca	aca	ctg	ggc	ttt	ggt	720	
Lys	Val	Leu	Val	Leu	Asn	Pro	Ser	Val	Ala	Ala	Thr	Leu	Gly	Phe	Gly		
225					230					235					240		
gct	tac	atg	tcc	aag	gct	cat	ggg	atc	gat	cct	aac	atc	agg	acc	ggg	768	
Ala	Tyr	Met	Ser	Lys	Ala	His	Gly	Ile	Asp	Pro	Asn	Ile	Arg	Thr	Gly		
				245					250					255			
gtg	aga	aca	att	acc	act	ggc	agc	ccc	atc	acg	tac	tcc	acc	tac	ggc	816	
Val	Arg	Thr	Ile	Thr	Thr	Gly	Ser	Pro	Ile	Thr	Tyr	Ser	Thr	Tyr	Gly		
			260					265					270				
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Lys	Phe	Leu	Ala	Asp	Gly	Gly	Cys	Ser	Gly	Gly	Ala	Tyr	Asp	Ile	Ile		
		275					280					285					
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	290					295					300						
ggc	act	gtc	ctt	gac	caa	gca	gag	act	gcg	ggg	gcg	aga	ctg	gtt	gtg	960	
Gly	Thr	Val	Leu	Asp	Gln	Ala	Glu	Thr	Ala	Gly	Ala	Arg	Leu	Val	Val		
305					310					315					320		
ctc	gcc	acc	gcc	acc	cct	ccg	ggc	tcc	gtc	act	gtg	ccc	cat	ccc	aac	1008	
Leu	Ala	Thr	Ala	Thr	Pro	Pro	Gly	Ser	Val	Thr	Val	Pro	His	Pro	Asn		
				325					330					335			
atc	gag	gag	gtt	gct	ctg	tcc	acc	acc	gga	gag	atc	cct	ttt	tac	ggc	1056	
Ile	Glu	Glu	Val	Ala	Leu	Ser	Thr	Thr	Gly	Glu	Ile	Pro	Phe	Tyr	Gly		
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Lys Ala Ile Pro Leu Glu Val Ile Lys Gly Gly Arg His Leu Ile Phe	
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tgt cat tca aag aag aag tgc gac gaa ctc gcc gca aag ctg gtc gca	1152
Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu Val Ala	
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Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val	
385 390 395 400	
atc ccg ccc atc ggc gat gtt gtc gtc gtg gca acc gat gcc ctc atg	1248
Ile Pro Pro Ile Gly Asp Val Val Val Val Ala Thr Asp Ala Leu Met	
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acc ggc tat acc ggc gac ttc gac tcg gtg ata gac tgc aat acg tgt	1296
Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Thr Cys	
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gtc acc cag aca gtc gat ttc agc ctt gac cct acc ttc acc att gag	1344
Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu	
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aca atc acg ctc ccc caa gat gct gtc tcc cgc act caa cgt cgg ggc	1392
Thr Ile Thr Leu Pro Gln Asp Ala Val Ser Arg Thr Gln Arg Arg Gly	
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agg act ggc agg ggg aag cca ggc atc tac aga ttt gtg gca ccg ggg	1440
Arg Thr Gly Arg Gly Lys Pro Gly Ile Tyr Arg Phe Val Ala Pro Gly	
465 470 475 480	
gag cgc ccc tcc ggc atg ttc gac tcg tcc gtc ctc tgt gag tgc tat	1488
Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu Cys Tyr	
485 490 495	
gac gca ggc tgt gct tgg tat gag ctc acg ccc gcc gag act aca gtt	1536
Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr Thr Val	
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agg cta cga gcg tac atg aac acc ccg ggg ctt ccc gtg tgc cag gac	1584
Arg Leu Arg Ala Tyr Met Asn Thr Pro Gly Leu Pro Val Cys Gln Asp	
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His Leu Glu Phe Trp Glu Gly Val Phe Thr Gly Leu Thr His Ile Asp	
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gcc cac ttt cta tcc cag aca aag cag agt ggg gag aac ctt cct tac	1680
Ala His Phe Leu Ser Gln Thr Lys Gln Ser Gly Glu Asn Leu Pro Tyr	
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Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro	

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Pro	Ser	Trp	Asp	Gln	Met	Trp	Lys	Cys	Leu	Ile	Arg	Leu	Lys	Pro	Thr															
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Leu	His	Gly	Pro	Thr	Pro	Leu	Leu	Tyr	Arg	Leu	Gly	Ala	Val	Gln	Asn															
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gaa	atc	acc	ctg	acg	cac	cca	gtc	acc	aaa	tac	atc	atg	aca	tgc	atg	1872														
Glu	Ile	Thr	Leu	Thr	His	Pro	Val	Thr	Lys	Tyr	Ile	Met	Thr	Cys	Met															
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Val	Leu	Ala	Ala	Leu	Ala	Ala	Tyr	Cys	Leu	Ser	Thr	Gly	Cys	Val	Val															
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Ile	Val	Gly	Arg	Val	Val	Leu	Ser	Gly	Lys	Pro	Ala	Ile	Ile	Pro	Asp															
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agg	gaa	gtc	ctc	tac	cga	gag	ttc	gat	gag	atg	gaa	gag	tgc			2058														
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675					680					685																				

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 <211> 686
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 representative NS3/4a conformational antigen

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 35 40 45
 Ile Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Thr Arg Thr
 50 55 60
 Ile Ala Ser Pro Lys Gly Pro Val Ile Gln Met Tyr Thr Asn Val Asp

65	70	75	80
Gln Asp Leu Val Gly Trp Pro Ala Pro Gln Gly Ser Arg Ser Leu Thr	85	90	95
Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala	100	105	110
Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu	115	120	125
Ser Pro Arg Pro Ile Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro Leu	130	135	140
Leu Cys Pro Ala Gly His Ala Val Gly Ile Phe Arg Ala Ala Val Cys	145	150	155
Thr Arg Gly Val Ala Lys Ala Val Asp Phe Ile Pro Val Glu Asn Leu	165	170	175
Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser Pro Pro	180	185	190
Val Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro Thr Gly	195	200	205
Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln Gly Tyr	210	215	220
Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly Phe Gly	225	230	235
Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg Thr Gly	245	250	255
Val Arg Thr Ile Thr Thr Gly Ser Pro Ile Thr Tyr Ser Thr Tyr Gly	260	265	270
Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Ile Ile	275	280	285
Ile Cys Asp Glu Cys His Ser Thr Asp Ala Thr Ser Ile Leu Gly Ile	290	295	300
Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val	305	310	315
Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His Pro Asn	325	330	335
Ile Glu Glu Val Ala Leu Ser Thr Thr Gly Glu Ile Pro Phe Tyr Gly	340	345	350
Lys Ala Ile Pro Leu Glu Val Ile Lys Gly Gly Arg His Leu Ile Phe			

355	360	365
Cys His Ser Lys Lys Lys	Cys Asp Glu Leu Ala	Ala Lys Leu Val Ala
370	375	380
Leu Gly Ile Asn Ala Val	Ala Tyr Tyr Arg Gly	Leu Asp Val Ser Val
385	390	395 400
Ile Pro Pro Ile Gly Asp	Val Val Val Val Ala	Thr Asp Ala Leu Met
405	410	415
Thr Gly Tyr Thr Gly Asp	Phe Asp Ser Val Ile	Asp Cys Asn Thr Cys
420	425	430
Val Thr Gln Thr Val Asp	Phe Ser Leu Asp Pro	Thr Phe Thr Ile Glu
435	440	445
Thr Ile Thr Leu Pro Gln	Asp Ala Val Ser Arg	Thr Gln Arg Arg Gly
450	455	460
Arg Thr Gly Arg Gly Lys	Pro Gly Ile Tyr Arg	Phe Val Ala Pro Gly
465	470	475 480
Glu Arg Pro Ser Gly Met	Phe Asp Ser Ser Val	Leu Cys Glu Cys Tyr
485	490	495
Asp Ala Gly Cys Ala Trp	Tyr Glu Leu Thr Pro	Ala Glu Thr Thr Val
500	505	510
Arg Leu Arg Ala Tyr Met	Asn Thr Pro Gly Leu	Pro Val Cys Gln Asp
515	520	525
His Leu Glu Phe Trp Glu	Gly Val Phe Thr Gly	Leu Thr His Ile Asp
530	535	540
Ala His Phe Leu Ser Gln	Thr Lys Gln Ser Gly	Glu Asn Leu Pro Tyr
545	550	555 560
Leu Val Ala Tyr Gln Ala	Thr Val Cys Ala Arg	Ala Gln Ala Pro Pro
565	570	575
Pro Ser Trp Asp Gln Met	Trp Lys Cys Leu Ile	Arg Leu Lys Pro Thr
580	585	590
Leu His Gly Pro Thr Pro	Leu Leu Tyr Arg Leu	Gly Ala Val Gln Asn
595	600	605
Glu Ile Thr Leu Thr His	Pro Val Thr Lys Tyr	Ile Met Thr Cys Met
610	615	620
Ser Ala Asp Leu Glu Val	Val Thr Ser Thr Trp	Val Leu Val Gly Gly
625	630	635 640
Val Leu Ala Ala Leu Ala	Ala Tyr Cys Leu Ser	Thr Gly Cys Val Val

	645		650		655
Ile Val Gly Arg Val Val Leu Ser Gly Lys Pro Ala Ile Ile Pro Asp					
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Arg Glu Val Leu Tyr Arg Glu Phe Asp Glu Met Glu Glu Cys					
	675		680		685

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 <212> DNA
 <213> Artificial Sequence

<220>
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Gly Ile Ile Asn Phe Glu Gln Lys Glu Ser Asn Gly Pro Val Lys Val	
20 25 30	
tgg gga agc att aaa gga ctg act gaa ggc ctg cat gga ttc cat gtt	144
Trp Gly Ser Ile Lys Gly Leu Thr Glu Gly Leu His Gly Phe His Val	
35 40 45	
cat gag ttt gga gat aat aca gca ggc tgt acc agt gca ggt cct cac	192
His Glu Phe Gly Asp Asn Thr Ala Gly Cys Thr Ser Ala Gly Pro His	
50 55 60	
ttt aat cct cta tcc acg cgt ggt tgc aat tgc tct atc tat ccc ggc	240
Phe Asn Pro Leu Ser Thr Arg Gly Cys Asn Cys Ser Ile Tyr Pro Gly	
65 70 75 80	
cat ata acg ggt cac cgc atg gca tgg aag ctt ggt tcc gcc gcc aga	288
His Ile Thr Gly His Arg Met Ala Trp Lys Leu Gly Ser Ala Ala Arg	
85 90 95	
act acc tcg ggc ttt gtc tcc ttg ttc gcc cca ggt gcc aaa caa aac	336
Thr Thr Ser Gly Phe Val Ser Leu Phe Ala Pro Gly Ala Lys Gln Asn	
100 105 110	
gaa act cac gtc acg gga ggc gca gcc gcc cga act acg tct ggg ttg	384
Glu Thr His Val Thr Gly Gly Ala Ala Ala Arg Thr Thr Ser Gly Leu	
115 120 125	

acc tct ttg ttc tcc cca ggt gcc agc caa aac att caa ttg att act	432
Thr Ser Leu Phe Ser Pro Gly Ala Ser Gln Asn Ile Gln Leu Ile Thr	
130 135 140	
agt acg gat aac tcc tct cca cca gta gtg ccc cag agc ttc cag gtg	480
Ser Thr Asp Asn Ser Ser Pro Pro Val Val Pro Gln Ser Phe Gln Val	
145 150 155 160	
gct cac ctc cat gct ccc aca ggc agc ggc aaa agc acc aag gtc ccg	528
Ala His Leu His Ala Pro Thr Gly Ser Gly Lys Ser Thr Lys Val Pro	
165 170 175	
gct gca tat gca gct cag ggc tat aag gtg cta gta ctc aac ccc tct	576
Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val Leu Val Leu Asn Pro Ser	
180 185 190	
gtt gct gca aca ctg ggc ttt ggt gct tac atg tcc aag gct cat ggg	624
Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr Met Ser Lys Ala His Gly	
195 200 205	
atc gat cct aac atc agg acc ggg gtg aga aca att acc act ggc agc	672
Ile Asp Pro Asn Ile Arg Thr Gly Val Arg Thr Ile Thr Thr Gly Ser	
210 215 220	
ccc atc acg tac tcc acc tac ggc aag ttc ctt gcc gac ggc ggg tgc	720
Pro Ile Thr Tyr Ser Thr Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys	
225 230 235 240	
tcg ggg ggc gct tat gac ata ata att tgt gac gag tgc cac tcc acg	768
Ser Gly Gly Ala Tyr Asp Ile Ile Ile Cys Asp Glu Cys His Ser Thr	
245 250 255	
gat gcc aca tcc atc ttg ggc atc ggc act gtc ctt gac caa gca gag	816
Asp Ala Thr Ser Ile Leu Gly Ile Gly Thr Val Leu Asp Gln Ala Glu	
260 265 270	
act gcg ggg gcg aga ctg gtt gtg ctc gcc acc gcc acc cct ccg ggc	864
Thr Ala Gly Ala Arg Leu Val Val Leu Ala Thr Ala Thr Pro Pro Gly	
275 280 285	
tcc gtc act gtg ccc cat ccc aac atc gag gag gtt gct ctg tcc acc	912
Ser Val Thr Val Pro His Pro Asn Ile Glu Glu Val Ala Leu Ser Thr	
290 295 300	
acc gga gag atc cct ttt tac ggc aag gct atc ccc ctc gaa gta atc	960
Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala Ile Pro Leu Glu Val Ile	
305 310 315 320	
aag ggg ggg aga cat ctc atc ttc tgt cat tca aag aag aag tgc gac	1008
Lys Gly Gly Arg His Leu Ile Phe Cys His Ser Lys Lys Lys Cys Asp	
325 330 335	
gaa ctc gcc gca aag ctg gtc gca ttg ggc atc aat gcc gtg gcc tac	1056
Glu Leu Ala Ala Lys Leu Val Ala Leu Gly Ile Asn Ala Val Ala Tyr	

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gtc gtg gca acc gat gcc ctc atg acc ggc tat acc ggc gac ttc gac Val Val Ala Thr Asp Ala Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp 370 375 380			1152
tcg gtg ata gac tgc aat acg tgt gca tgc tcc ggg aag ccg gca atc Ser Val Ile Asp Cys Asn Thr Cys Ala Cys Ser Gly Lys Pro Ala Ile 385 390 395 400			1200
ata cct gac agg gaa gtc ctc tac cga gag ttc gat gag atg gaa gag Ile Pro Asp Arg Glu Val Leu Tyr Arg Glu Phe Asp Glu Met Glu Glu 405 410 415			1248
tgc tct cag cac tta ccg tac atc gag caa ggg atg atg ctc gcc gag Cys Ser Gln His Leu Pro Tyr Ile Glu Gln Gly Met Met Leu Ala Glu 420 425 430			1296
cag ttc aag cag aag gcc ctc ggc ctc tcg cga ggg ggc aag ccg gca Gln Phe Lys Gln Lys Ala Leu Gly Leu Ser Arg Gly Gly Lys Pro Ala 435 440 445			1344
atc gtt cca gac aaa gag gtg ttg tat caa caa tac gat gag atg gaa Ile Val Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu 450 455 460			1392
gag tgc tca caa gct gcc cca tat atc gaa caa gct cag gta ata gct Glu Cys Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala 465 470 475 480			1440
cac cag ttc aag gaa aaa gtc ctt gga ttg atc gat aat gat caa gtg His Gln Phe Lys Glu Lys Val Leu Gly Leu Ile Asp Asn Asp Gln Val 485 490 495			1488
gtt gtg act cct gac aaa gaa atc tta tat gag gcc ttt gat gag atg Val Val Thr Pro Asp Lys Glu Ile Leu Tyr Glu Ala Phe Asp Glu Met 500 505 510			1536
gaa gaa tgc gcc tcc aaa gcc gcc ctc att gag gaa ggg cag cgg atg Glu Glu Cys Ala Ser Lys Ala Ala Leu Ile Glu Glu Gly Gln Arg Met 515 520 525			1584
gcg gag atg ctc aag tct aag ata caa ggc ctc ctc ggg ata ctg cgc Ala Glu Met Leu Lys Ser Lys Ile Gln Gly Leu Leu Gly Ile Leu Arg 530 535 540			1632
cgg cac gtt ggt cct ggc gag ggg gca gtg cag tgg atg aac cgg ctg Arg His Val Gly Pro Gly Glu Gly Ala Val Gln Trp Met Asn Arg Leu 545 550 555 560			1680

ata gcc ttc gcc tcc aga ggg aac cat gtt tcc ccc acg cac tac gtt	1728
Ile Ala Phe Ala Ser Arg Gly Asn His Val Ser Pro Thr His Tyr Val	
565 570 575	
ccg tct aga tcc cgg aga ttc gcc cag gcc ctg ccc gtt tgg gcg cgg	1776
Pro Ser Arg Ser Arg Arg Phe Ala Gln Ala Leu Pro Val Trp Ala Arg	
580 585 590	
ccg gac tat aac ccc ccg cta gtg gag acg tgg aaa aag ccc gac tac	1824
Pro Asp Tyr Asn Pro Pro Leu Val Glu Thr Trp Lys Lys Pro Asp Tyr	
595 600 605	
gaa cca cct gtg gtc cac ggc aga tct tct cgg aga ttc gcc cag gcc	1872
Glu Pro Pro Val Val His Gly Arg Ser Ser Arg Arg Phe Ala Gln Ala	
610 615 620	
ctg ccc gtt tgg gcg cgg ccg gac tat aac ccc ccg cta gtg gag acg	1920
Leu Pro Val Trp Ala Arg Pro Asp Tyr Asn Pro Pro Leu Val Glu Thr	
625 630 635 640	
tgg aaa aag ccc gac tac gaa cca cct gtg gtc cat ggc aga aag acc	1968
Trp Lys Lys Pro Asp Tyr Glu Pro Pro Val Val His Gly Arg Lys Thr	
645 650 655	
aaa cgt aac acc aac cgg cgg ccg cag gac gtc aag ttc ccg ggt ggc	2016
Lys Arg Asn Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly	
660 665 670	
ggg cag atc gtt ggt gga gtt tac ttg ttg ccg cgc agg ggc cct aga	2064
Gly Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg	
675 680 685	
ttg ggt gtg ctc gcg acg aga aag act tcc cct atc ccc aag gct cgt	2112
Leu Gly Val Leu Ala Thr Arg Lys Thr Ser Pro Ile Pro Lys Ala Arg	
690 695 700	
cgg ccc gag ggc agg acc tgg gct cag ccc ggt tac cct tgg ccc ctc	2160
Arg Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly Tyr Pro Trp Pro Leu	
705 710 715 720	
tat ggc aat aag gac aga cgg tct aca ggt aag tcc tgg ggt aag cca	2208
Tyr Gly Asn Lys Asp Arg Arg Ser Thr Gly Lys Ser Trp Gly Lys Pro	
725 730 735	
ggg tac cct tgg cca aga aag acc aaa cgt aac acc aac cgg cgg ccg	2256
Gly Tyr Pro Trp Pro Arg Lys Thr Lys Arg Asn Thr Asn Arg Arg Pro	
740 745 750	
cag gac gtc aag ttc ccg ggt ggc ggt cag atc gtt ggt gga gtt tac	2304
Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly Gly Val Tyr	
755 760 765	
ttg ttg ccg cgc agg ggc cct aga ttg ggt gtg ctc gcg acg aga aag	2352
Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Leu Ala Thr Arg Lys	

770	775	780	
act tcc cct atc ccc aag gct cgt cgg ccc gag ggc agg acc tgg gct			2400
Thr Ser Pro Ile Pro Lys Ala Arg Arg Pro Glu Gly Arg Thr Trp Ala			
785	790	795	800
cag ccc ggt tac cct tgg ccc ctc tat ggc aat aag gac aga cgg tct			2448
Gln Pro Gly Tyr Pro Trp Pro Leu Tyr Gly Asn Lys Asp Arg Arg Ser			
	805	810	815
aca ggt aag tcc tgg ggt aag cca ggg tac cct tgg ccc taatgagtcg ac			2499
Thr Gly Lys Ser Trp Gly Lys Pro Gly Tyr Pro Trp Pro			
	820	825	

<210> 5
 <211> 829
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: MEFA 12

<400> 5
 Met Ala Thr Lys Ala Val Cys Val Leu Lys Gly Asp Gly Pro Val Gln
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 Gly Ile Ile Asn Phe Glu Gln Lys Glu Ser Asn Gly Pro Val Lys Val
 20 25 30
 Trp Gly Ser Ile Lys Gly Leu Thr Glu Gly Leu His Gly Phe His Val
 35 40 45
 His Glu Phe Gly Asp Asn Thr Ala Gly Cys Thr Ser Ala Gly Pro His
 50 55 60
 Phe Asn Pro Leu Ser Thr Arg Gly Cys Asn Cys Ser Ile Tyr Pro Gly
 65 70 75 80
 His Ile Thr Gly His Arg Met Ala Trp Lys Leu Gly Ser Ala Ala Arg
 85 90 95
 Thr Thr Ser Gly Phe Val Ser Leu Phe Ala Pro Gly Ala Lys Gln Asn
 100 105 110
 Glu Thr His Val Thr Gly Gly Ala Ala Ala Arg Thr Thr Ser Gly Leu
 115 120 125
 Thr Ser Leu Phe Ser Pro Gly Ala Ser Gln Asn Ile Gln Leu Ile Thr
 130 135 140
 Ser Thr Asp Asn Ser Ser Pro Pro Val Val Pro Gln Ser Phe Gln Val
 145 150 155 160

Ala His Leu His Ala Pro Thr Gly Ser Gly Lys Ser Thr Lys Val Pro
 165 170 175

Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val Leu Val Leu Asn Pro Ser
 180 185 190

Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr Met Ser Lys Ala His Gly
 195 200 205

Ile Asp Pro Asn Ile Arg Thr Gly Val Arg Thr Ile Thr Thr Gly Ser
 210 215 220

Pro Ile Thr Tyr Ser Thr Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys
 225 230 235 240

Ser Gly Gly Ala Tyr Asp Ile Ile Ile Cys Asp Glu Cys His Ser Thr
 245 250 255

Asp Ala Thr Ser Ile Leu Gly Ile Gly Thr Val Leu Asp Gln Ala Glu
 260 265 270

Thr Ala Gly Ala Arg Leu Val Val Leu Ala Thr Ala Thr Pro Pro Gly
 275 280 285

Ser Val Thr Val Pro His Pro Asn Ile Glu Glu Val Ala Leu Ser Thr
 290 295 300

Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala Ile Pro Leu Glu Val Ile
 305 310 315 320

Lys Gly Gly Arg His Leu Ile Phe Cys His Ser Lys Lys Lys Cys Asp
 325 330 335

Glu Leu Ala Ala Lys Leu Val Ala Leu Gly Ile Asn Ala Val Ala Tyr
 340 345 350

Tyr Arg Gly Leu Asp Val Ser Val Ile Pro Thr Ser Gly Asp Val Val
 355 360 365

Val Val Ala Thr Asp Ala Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp
 370 375 380

Ser Val Ile Asp Cys Asn Thr Cys Ala Cys Ser Gly Lys Pro Ala Ile
 385 390 395 400

Ile Pro Asp Arg Glu Val Leu Tyr Arg Glu Phe Asp Glu Met Glu Glu
 405 410 415

Cys Ser Gln His Leu Pro Tyr Ile Glu Gln Gly Met Met Leu Ala Glu
 420 425 430

Gln Phe Lys Gln Lys Ala Leu Gly Leu Ser Arg Gly Gly Lys Pro Ala
 435 440 445

Ile Val Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu
 450 455 460
 Glu Cys Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala
 465 470 475 480
 His Gln Phe Lys Glu Lys Val Leu Gly Leu Ile Asp Asn Asp Gln Val
 485 490 495
 Val Val Thr Pro Asp Lys Glu Ile Leu Tyr Glu Ala Phe Asp Glu Met
 500 505 510
 Glu Glu Cys Ala Ser Lys Ala Ala Leu Ile Glu Glu Gly Gln Arg Met
 515 520 525
 Ala Glu Met Leu Lys Ser Lys Ile Gln Gly Leu Leu Gly Ile Leu Arg
 530 535 540
 Arg His Val Gly Pro Gly Glu Gly Ala Val Gln Trp Met Asn Arg Leu
 545 550 555 560
 Ile Ala Phe Ala Ser Arg Gly Asn His Val Ser Pro Thr His Tyr Val
 565 570 575
 Pro Ser Arg Ser Arg Arg Phe Ala Gln Ala Leu Pro Val Trp Ala Arg
 580 585 590
 Pro Asp Tyr Asn Pro Pro Leu Val Glu Thr Trp Lys Lys Pro Asp Tyr
 595 600 605
 Glu Pro Pro Val Val His Gly Arg Ser Ser Arg Arg Phe Ala Gln Ala
 610 615 620
 Leu Pro Val Trp Ala Arg Pro Asp Tyr Asn Pro Pro Leu Val Glu Thr
 625 630 635 640
 Trp Lys Lys Pro Asp Tyr Glu Pro Pro Val Val His Gly Arg Lys Thr
 645 650 655
 Lys Arg Asn Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly
 660 665 670
 Gly Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg
 675 680 685
 Leu Gly Val Leu Ala Thr Arg Lys Thr Ser Pro Ile Pro Lys Ala Arg
 690 695 700
 Arg Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly Tyr Pro Trp Pro Leu
 705 710 715 720
 Tyr Gly Asn Lys Asp Arg Arg Ser Thr Gly Lys Ser Trp Gly Lys Pro
 725 730 735

Gly Tyr Pro Trp Pro Arg Lys Thr Lys Arg Asn Thr Asn Arg Arg Pro
740 745 750

Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly Gly Val Tyr
755 760 765

Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Leu Ala Thr Arg Lys
770 775 780

Thr Ser Pro Ile Pro Lys Ala Arg Arg Pro Glu Gly Arg Thr Trp Ala
785 790 795 800

Gln Pro Gly Tyr Pro Trp Pro Leu Tyr Gly Asn Lys Asp Arg Arg Ser
805 810 815

Thr Gly Lys Ser Trp Gly Lys Pro Gly Tyr Pro Trp Pro
820 825

<210> 6
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: consensus
sequence from HCV type 1 genome

<400> 6
Gly Ser Ala Ala Arg Thr Thr Ser Gly Phe Val Ser Leu Phe Ala Pro
1 5 10 15

Gly Ala Lys Gln Asn
20

<210> 7
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: sequence

<400> 7
acaaaacaaa 10

<210> 8
<211> 23
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: NS4A peptide

<400> 8

Lys	Lys	Gly	Ser	Val	Val	Ile	Val	Gly	Arg	Ile	Val	Leu	Ser	Gly	Lys
1				5				10					15		

Pro	Ala	Ile	Ile	Pro	Lys	Lys
			20			